

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: May 18, 2002, 05:12:35 ; Search time 42:56 Seconds
(without alignments)
239.268 Million cell updates/sec

Title: US-09-719-748-2_COPY_13_275

Perfect score: 1343
Sequence: 1 YDIGELGSGQFAIVKKCRE.....LVKTRKRLTIOEALRHPWI 263

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues

Initial number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database : SwissProt_40.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1124	83.7	1431	1	DAPK_HUMAN
2	653.5	48.7	1176	1	KMLS_BOVIN
3	647.5	48.2	1906	1	KMLS_CHICK
4	642.5	47.8	1914	1	KMLS_HUMAN
5	639	47.6	397	1	S17A_RABIT
6	638	47.5	414	1	S17A_RABIT
7	636.5	47.4	1147	1	KMLS_HUMAN
8	625	46.5	372	1	S17B_HUMAN
9	611.5	45.5	438	1	KMLS_SHEEP
10	571.5	42.6	607	1	KMLS_RABIT
11	570.5	42.5	609	1	KMLS_RABIT
12	530.5	37.9	285	1	KMLC_DICDI
13	509	37.9	473	1	KCCG_HUMAN
14	506	37.7	474	1	KCCG_HUMAN
15	505	37.6	469	1	KCCG_HUMAN
16	500	37.2	3038	1	TRIO_HUMAN
17	495	36.9	533	1	KCCD_RAT
18	488	36.3	489	1	KCCD_HUMAN
19	485	36.1	370	1	KCCI_HUMAN
20	485	36.0	374	1	KCCI_RAT
21	483.5	36.0	424	1	KPSH_HUMAN
22	483	36.0	542	1	CDP3_ORYSA
23	480	35.7	533	1	CDP2_ORYSA
24	479.5	35.7	740	1	DCK1_HUMAN
25	478.5	35.6	433	1	DCK1_HUMAN
26	478.5	35.6	756	1	DCK1_RAT
27	475	35.4	478	1	KCCA_RAT
28	471	35.1	478	1	KCCA_MOUSE
29	469	34.9	527	1	KCCG_RAT
30	468	34.8	532	1	CDPK_DAUCA
31	468	34.8	610	1	CDP1_ARATH
32	464	34.5	534	1	CDP1_ORYSA
33	462	34.4	508	1	CDPK_SOYBN

34	462	34.4	513	1	CDP2_MAIZE
35	460	34.3	542	1	KCCB_MOUSE
36	459	34.2	335	1	KCCI_SCHPO
37	458	34.1	512	1	KIIO_ARATH
38	457	34.0	542	1	KCCB_RAT
39	457	34.0	664	1	KCCB_HUMAN
40	456.5	34.0	406	1	KPBH_RAT
41	452.5	33.7	406	1	KPBH_HUMAN
42	452	33.7	386	1	KPBG_RABIT
43	450	33.5	909	1	CSRP_RAT
44	450	33.5	921	1	CSRP_HUMAN
45	450	33.5	924	1	CSRP_MOUSE

ALIGNMENTS

RESULT 1	DAPK_HUMAN	STANDARD;	PRT; 1431 AA.
ID	DAPK_HUMAN		
AC	P53355;		
DT	01-OCT-1996 (Rel. 34, Created)		
DT	01-NOV-1997 (Rel. 35, Last sequence update)		
DT	16-OCT-2001 (Rel. 40, Last annotation update)		
DE	Death-associated protein kinase 1 (EC 2.7.1.1) (DAP kinase 1).		
GN	DAPK1 OR DAPK.		
OS	Homo sapiens (Human).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
OX	NCBI_Taxid=9606;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RX	MEDLINE=95129831; Pubmed=7828849;		
RA	Deiss L.P., Feinstein E., Berissi H., Cohen O., Kimchi A.;		
RT	"Identification of a novel serine/threonine kinase and a novel 15-kD		
RT	protein as potential mediators of the gamma interferon-induced cell		
RT	death.";		
RL	Genes Dev. 9:15-30(1995).		
RN	[2]		
RP	REVISIONS TO 164-171.		
RA	Feinstein E.;		
RL	Submitted (APR-1997) to the EMBL/GenBank/DBJ databases.		
CC	-1- FUNCTION: INVOLVED IN MEDIATING INTERFERON-GAMMA-INDUCED CELL		
CC	DEATH.		
CC	-1- PFM: AUTOPHOSPHORYLATED.		
CC	-1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.		
CC	-1- SIMILARITY: CONTAINS 10 ANK REPEATS.		
CC	-1- SIMILARITY: CONTAINS 1 DEATH DOMAIN.		
CC	-----		
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CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/		
CC	or send an email to license@isb-sib.ch).		
CC	-----		
DR	EMBL: X76104; CA53712.1; -		
DR	HSSP: 063450; 1A06.		
DR	MIM: 600831; -		
DR	InterPro: IPR002110; ANK.		
DR	InterPro: IPR000488; Death.		
DR	InterPro: IPR000719; Euk. kinase.		
DR	InterPro: IPR002290; Ser_thr_kinase.		
DR	Pfam: PF00023; ank; 8.		
DR	Pfam: PF00531; death; 1.		
DR	Pfam: PF00069; pkinase; 1.		
DR	SMART: SM00248; ANK; 7.		
DR	SMART: SM00005; DEATH; 1.		
DR	SMART: SM00220; S_TKC; 1.		
DR	PROSITE: PS50088; ANK_REPEAT; 6.		
DR	PROSITE: PS50297; ANK_REPEAT_REGION; 1.		
DR	PROSITE: PS50017; DEATH_DOMAIN; 1.		

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DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE: PS00108; PROTEIN_KINASE_DOM; 1.
 DR Trifunctional: Serine/threonine-protein kinase; Calmodulin-binding;
 KM Phosphorylation; ATP-binding; Repeat; ANK repeat; Apoptosis.
 FT DOMAIN 13 266
 FT REPEAT 267 334 CALMODULIN-BINDING.
 FT REPEAT 378 407 ANK 1.
 FT REPEAT 411 440 ANK 2.
 FT REPEAT 444 473 ANK 3.
 FT REPEAT 478 507 ANK 4.
 FT REPEAT 511 540 ANK 5.
 FT REPEAT 544 573 ANK 6.
 FT REPEAT 577 606 ANK 7.
 FT REPEAT 610 639 ANK 8.
 FT REPEAT 876 905 ANK 9.
 FT REPEAT 1163 1197 ANK 10.
 FT DOMAIN 1313 1397 DEATH.
 FT NP_BIND 19 27 ATP (BY SIMILARITY).
 FT BINDING 42 42 ATP (BY SIMILARITY).
 FT ACT_SITE 139 139 BY SIMILARITY.
 FT MUTAGEN 42 42 R->A: LOSS OF ACTIVITY.
 SQ SEQUENCE 1431 AA; 160017 MW; 9EE64811004A155B CRC64;

Query Match 83.7%; Score 1124; DB 1; Length 1431;
 Best Local Similarity 79.5%; Pred. No. 5,8e-65;
 Matches 209; Conservative 41; Mismatches 13; Indels 0; Gaps 0;

QY 1 YVIGELSGGQFAIVKCKEKGLEYAKFKKRSRGRVSGEETREVSILROYL 60
 DB 13 YVIGELSGGQFAIVKCKEKGLEYAKFKKRSRGRVSGEETREVSILROYL 60
 QY 61 HHNVITLHDVYENRDEYVHILELVSGLGELFLAOKESSEETATFIOIIGVYLT 120
 DB 73 HHNVITLHDVYENRDEYVHILELVSGLGELFLAOKESSEETATFIOIIGVYLT 120
 QY 121 KRIAHFDLKPENIMLDKNIPPIPHKILDFGLAHEIEDGVVERKNIPTPEFVAPELVN 180
 DB 133 LOIAHFDLKPENIMLDKNIPPIPHKILDFGLAHEIEDGVVERKNIPTPEFVAPELVN 180
 QY 181 PIGLEADMSIGVITYILLSGASPLFGDVKOETLANITVSVDPEEFSSHTSELAKEFI 240
 DB 193 PIGLEADMSIGVITYILLSGASPLFGDVKOETLANITVSVDPEEFSSHTSELAKEFI 240
 QY 241 RRLVETKRLTIOEALRHPI 263
 DB 253 RRLVETKRLTIOEALRHPI 263
 KMLS_BOVIN 2
 ID KMLS_BOVIN STANDARD; PRT: 1176 AA.
 AC Q28824;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Myosin light chain kinase, smooth muscle (EC 2.7.1.117) (MCK)
 DE [Contains: Telokin].
 GN MYLK.
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Bovinae; Bos.
 OC NCBI_TaxID=9913;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Stomach;
 RA MEDLINE=93203148; PubMed=1284247;
 RA Kobayashi H., Inoue A., Mikawa T., Kuwayama H., Hotta Y., Masaki T.,
 RA Ebashi S.;
 RT "Isolation of cDNA for bovine stomach 155 kDa protein exhibiting
 RT myosin light chain kinase activity.";

RL J. Blochem. 112:786-791(1992).
 CC -1- FUNCTION: CALCIUM/CALMODULIN-DEPENDENT ENZYME RESPONSIBLE FOR
 CC SMOOTH MUSCLE CONTRACTION VIA PHOSPHORYLATION OF A SPECIFIC SERINE
 CC IN THE N-TERMINUS OF MYOSIN LIGHT CHAINS (MLC). AN EVENT THAT
 CC FACILITATES MYOSIN INTERACTION WITH ACTIN FILAMENTS.
 CC -1- CATALYTIC ACTIVITY: ATP + [myosin light-chain] = ADP + [myosin
 CC light-chain] phosphate.
 CC -1- SUBUNIT: TELOKIN BINDS CALMODULIN.
 CC -1- ALTERNATIVE PRODUCTS: AT LEAST 3 ISOMERISMS OF MCK ARE PRODUCED BY
 CC ALTERNATIVE INITIATION. A NON-MUSCLE FORM (WHICH IS THE LONGEST
 CC FORM); A SMOOTH-MUSCLE FORM AND TELOKIN (A C-TERMINAL SECTION WITH
 CC NO CATALYTIC ACTIVITY).
 CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
 CC -1- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.
 CC -1- SIMILARITY: CONTAINS 1 FIBRONECTIN TYPE III-LIKE DOMAIN.
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 CC -----
 CC EMBL: S57131; AAB25794.1; .
 CC HSP: P56276; IRLK.
 DR InterPro: IPR000719; Euk_pkinase.
 DR InterPro: IPR003961; FN_III.
 DR InterPro: IPR003006; I9_MHC.
 DR InterPro: IPR003598; I9_C2.
 DR InterPro: IPR003600; I9_1like.
 DR InterPro: IPR002290; Ser_thr_pkinase.
 DR Pfam: PF00047; fn3; 1.
 DR Pfam: PF00047; I9; 2.
 DR Pfam: PF00069; pkinase; 1.
 DR SMART: SM00060; FN3; 1.
 DR SMART: SM00410; IG_1like; 1.
 DR SMART: SM00408; IG2; 2.
 DR SMART: SM00220; S_TKC; 1.
 DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE: PS00108; PROTEIN_KINASE_DOM; 1.
 DR Trifunctional: Serine/threonine-protein kinase; Calmodulin-binding;
 DR ATP-binding; Phosphorylation; Immunoglobulin domain; Repeat;
 DR Alternative Initiation.
 DR CHAIN 1 1176
 FT CHAIN 1022 1176
 FT INIT_MET 1022 1022
 FT DOMAIN 100 291
 FT REPEAT 100 111
 FT REPEAT 112 123
 FT REPEAT 124 135
 FT REPEAT 136 147
 FT REPEAT 148 159
 FT REPEAT 160 171
 FT REPEAT 172 183
 FT REPEAT 184 195
 FT REPEAT 196 207
 FT REPEAT 208 219
 FT REPEAT 220 231
 FT REPEAT 232 243
 FT REPEAT 244 255
 FT REPEAT 256 267
 FT REPEAT 268 279
 FT REPEAT 280 291
 FT DOMAIN 603 673
 FT DOMAIN 725 780
 FT DOMAIN 972 1035
 FT DOMAIN 1084 1151
 FT NP_BIND 731 739
 FT BINDING 754 754
 FT ACT_SITE 846 846
 MYOSIN LIGHT CHAIN KINASE, SMOOTH-MUSCLE
 ISOZYME.
 TELOKIN.
 16 x 12 AA TANDEM REPEATS.
 1.
 2.
 3 (INCOMPLETE).
 4.
 5.
 6.
 7.
 8.
 9.
 10.
 11.
 12.
 13.
 14.
 15.
 16.
 FIBRONECTIN TYPE-III.
 PROTEIN KINASE.
 CALMODULIN-BINDING.
 IG-LIKE C2-TYPE DOMAIN.
 ATP (BY SIMILARITY).
 ATP (BY SIMILARITY).
 BY SIMILARITY.

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